

1 TTTCCTCACTGACTATAAAGAATAGAGAAGGAGGCTTCAGTGACCGGCTGCTGGCTGACTTACAGCAGTCAGACTCTGACAGATC
91 ATGGCTATGATGAGGTCAGGGGGGAGCCAGCCCTGGGACAGACCCTGCGTCTGATCGTATCTTCAAGTGGCTCCGAGTCTCTCTGT
1 MetAlaMetMetGluValGlnGlyProSerLeuGlnThrCysValLeuIleValIlePheThrValLeuLeuGlnSerLeuCys
1 GTGGCTGTAACCTTACCGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAGTGCGCATTTGCTTCTTAAAGAA
1 ValAlaValIleThrTyrValTyrPheThrAsnGlnLeuLysGlnMetGlnAspLysTyrSerLysSerGlyIleAlaCysPheLeuLysGlu
271 GATGACAGTTATTGGGACCCCAATGACGAGAAGAGTATGAACAGCCCTGCTGGCAAGTCAAGTGCGCAACTCCGCTCAGCTCGTTAGAAAG
61 AspAspSerTyrTrpAspProAsnAspGluGlnSerMetAsnSerProCysTrpGlnValLysTrpGlnLeuValArgGlnLeuValArgLys
361 ATGATTTTGAGAACCTCTGAGGAACCAATTCTTACAGTTCAGAAAGCAACAATAATTCTCCCTAGTGAGAGAGAAGAGTCCNCAG
91 MetIleLeuArgThrSerGlnGluThrIleSerThrValGlnGlnLysGlnGlnAsnIleSerProLeuValArgGluArgGlyProGln
451 AGAGTAGCAGCTCACATAACTGGGACCCAGAGAGAAGCAACACATTGCTCTTCCAAACTCCAGAAGATGAAAGGCTCTGGGCCGCAAA
121 ArgValAlaAlaHisIleThrGlyThrArgGlyArgSerAsnThrLeuSerSerProAsnSerLysAsnGlnLysAlaLeuGlyArgLys
541 ATAAACTCCTGGGAATCATCAAGAGTGGGCATTCTCATTCCTGAGCAACTTGCACCTTGAGGAATGGTGAACCTGGTCATCCATGAATAAGG
151 IleAsnSerTrpGlnSerSerArgSerGlyHisSerPheLeuSerAsnLeuHisLeuArgAsnGlyGluLeuValIleHisGlnLysGly
631 TTTTACTACATCTATTCCCAACATACTTTCGATTTCAGAGAGAAATAAAGAAACACAAAGACGACAACAATGCTCCAATATATT
181 PheTyrTyrIleTyrSerGlnThrTyrPheArgPheGlnGlnIleLysGlnAsnThrLysAsnAspLysGlnMetValGlnTyrIle
721 TACAATATACACAAGTTATCCCTGACCCCTATATTGTTGATGAAGAAAGTGCTAGAAATAGTTGTTGCTTAAGATGCAGAATATGACTCTAT
111 TyrLysTyrThrSerTyrProAspProIleLeuLeuMetLysSerAlaArgAsnSerCysTrpSerLysAspAlaGlnTyrGlyLeuTyr
241 TCCATCTATCAAGGGGAAATATTGAGGCTTAAGGAAATGACAGAAATTTTGTCTCTGTAACAATGAGCACTTGATAGACATGAGCCAT
111 SerIleTyrGlnGlyIlePheGlnLeuLysGlnAsnAspArgIlePheValSerValThrAsnGlnHisLeuIleAspMetAspHis
901 GAAGCCAGTTTTCGGGGCTTTTGTAGTTGGCTAACTGACCTGGAAGAAAGCAATAACCTCAAGTGAAGTACTATTCACTTTTCAGGAT
271 GluAlaSerPhePheGlyAlaPheLeuValGlyStp
991 GATACACTATGAAGATGTTTCAAAAAATCTGACCAAAACAACAACAGAAA

FIG. 1

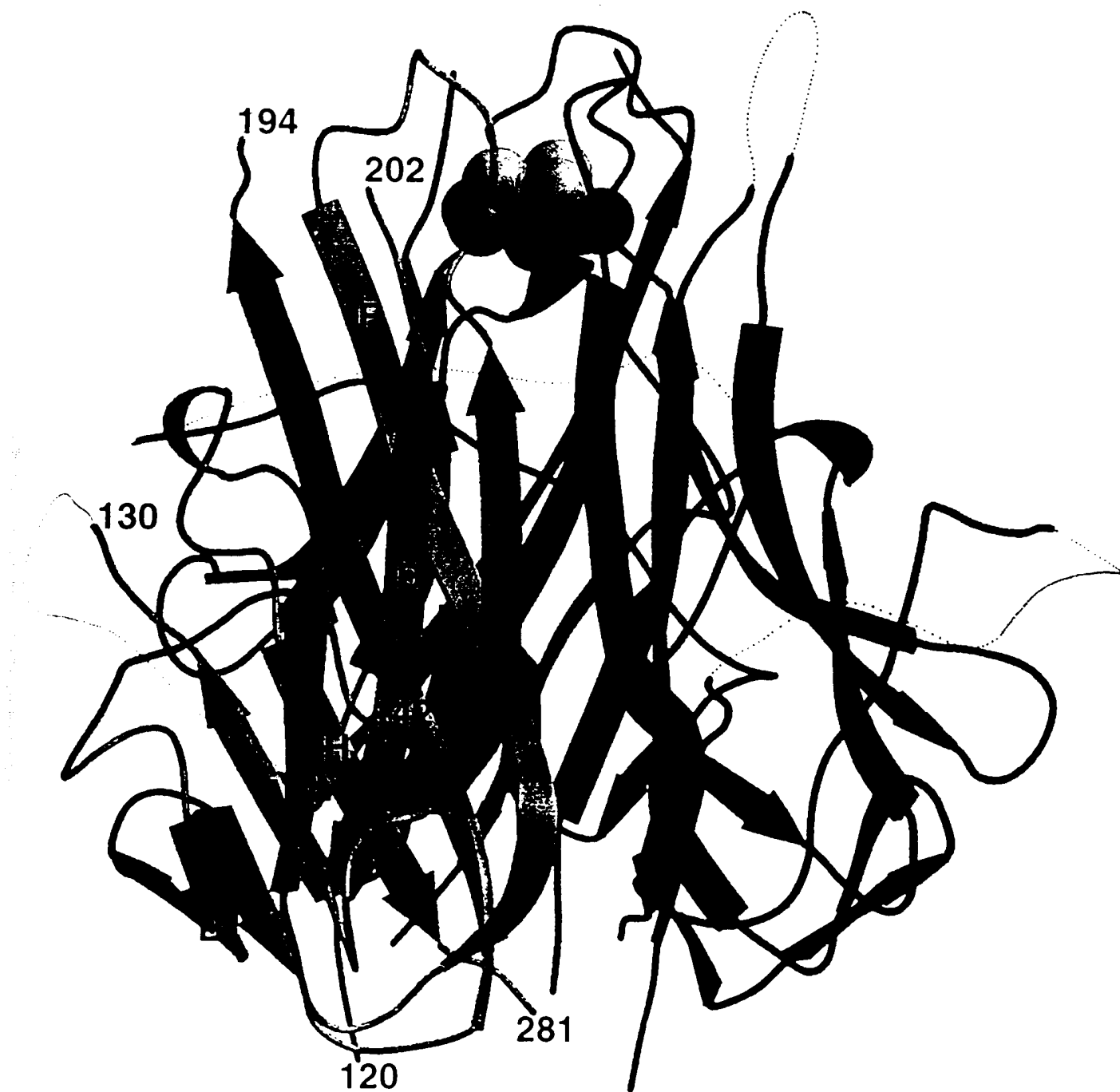


Figure 2A



Figure 2B

Crystallographic Data			
	<u>ApC-2L(114-281)</u>	<u>ApC-2L(91-281) D218A</u>	<u>ApC-2L(91-281) D218A</u>
Crystal			
Space Group	P6 ₃	R32	R32
Unit Cell (Å)	a=72.5 c=140	a=66.4 c=197.6	a=66.4 c=197.7
Resolution (Å)	3.9	1.9	1.3
Coverage (%)	94 (96)	93 (99)	100 (100)
<I/σ(I)>	5.9	10.1	12.4
# unique (hkl)	3589	12680	41840
redundancy	4.9	4.3	12.1
R _{symm} (%)	15.4 (34)	6.2 (27)	6.4 (34)
# protomers in ASU	2	1	1
Refinement			
R _{cryst} (%)	33.8	20	
R _{free} (%)	27.6	22	
rmsd bonds (Å)	0.009	0.015	0.007
rmsd angles (°)	1.79	2.0	1.41
average B-values	--	14	14
# water molecules	0	170	

$R_{\text{symm}} = \sum_h \sum_i (I_{hi} - \langle I_h \rangle) / \sum_h I$ where I_h is the mean structure factor intensity of i observations of symmetry-related reflections with Bragg index h . $R_{\text{cryst}} = (\sum_h \sum_i |F_{\text{obs}}| - |F_{\text{calc}}|) / \sum_i |F_{\text{obs}}|$ where F_{obs} and F_{calc} are the observed and calculated structure factor amplitudes. $R_{\text{free}} = \sum_{(hkl) \in \tau} |F_{\text{obs}}(hkl)| - k|F(hkl)| / \sum_{(hkl) \in \tau} |F_{\text{obs}}(hkl)|$ where the τ set of reflections is omitted from the refinement process. 10% of the data were included in the τ set for calculation of R_{free} and not included in refinement. Values in parenthesis are for the highest resolution shell.

Fig. 2C

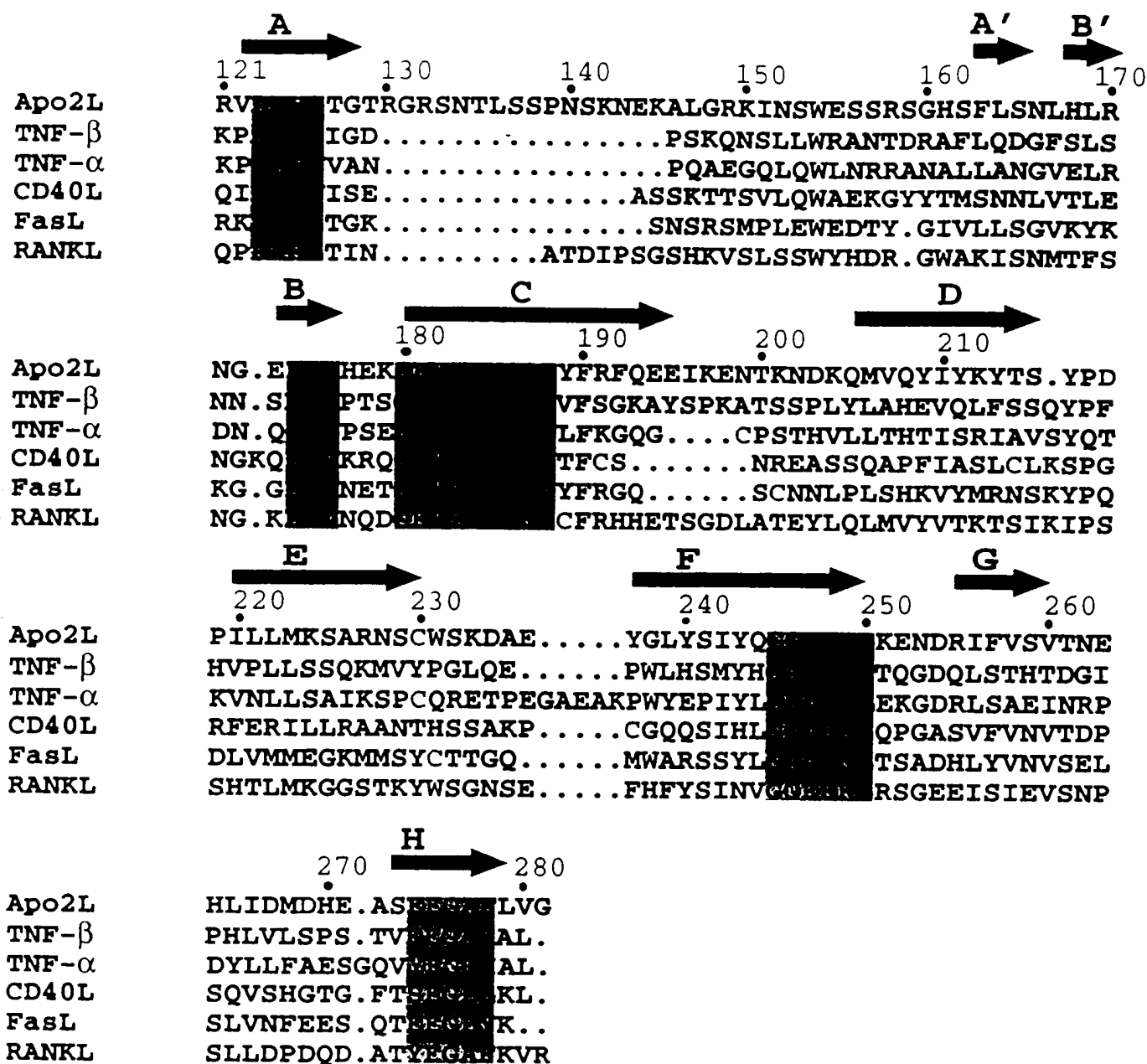


Figure 3

Relative Fluorescence Units
(RFU)

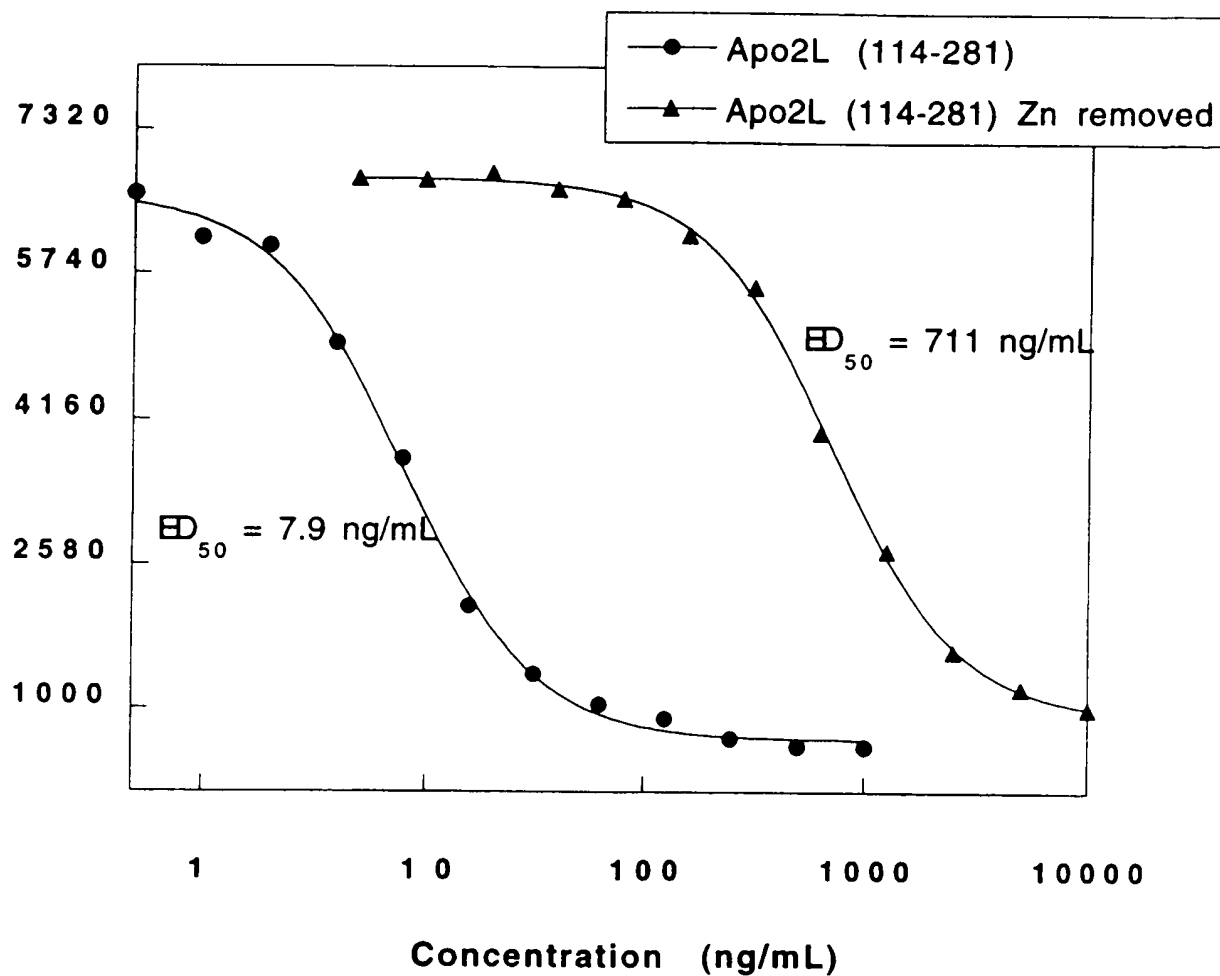


Fig. 4

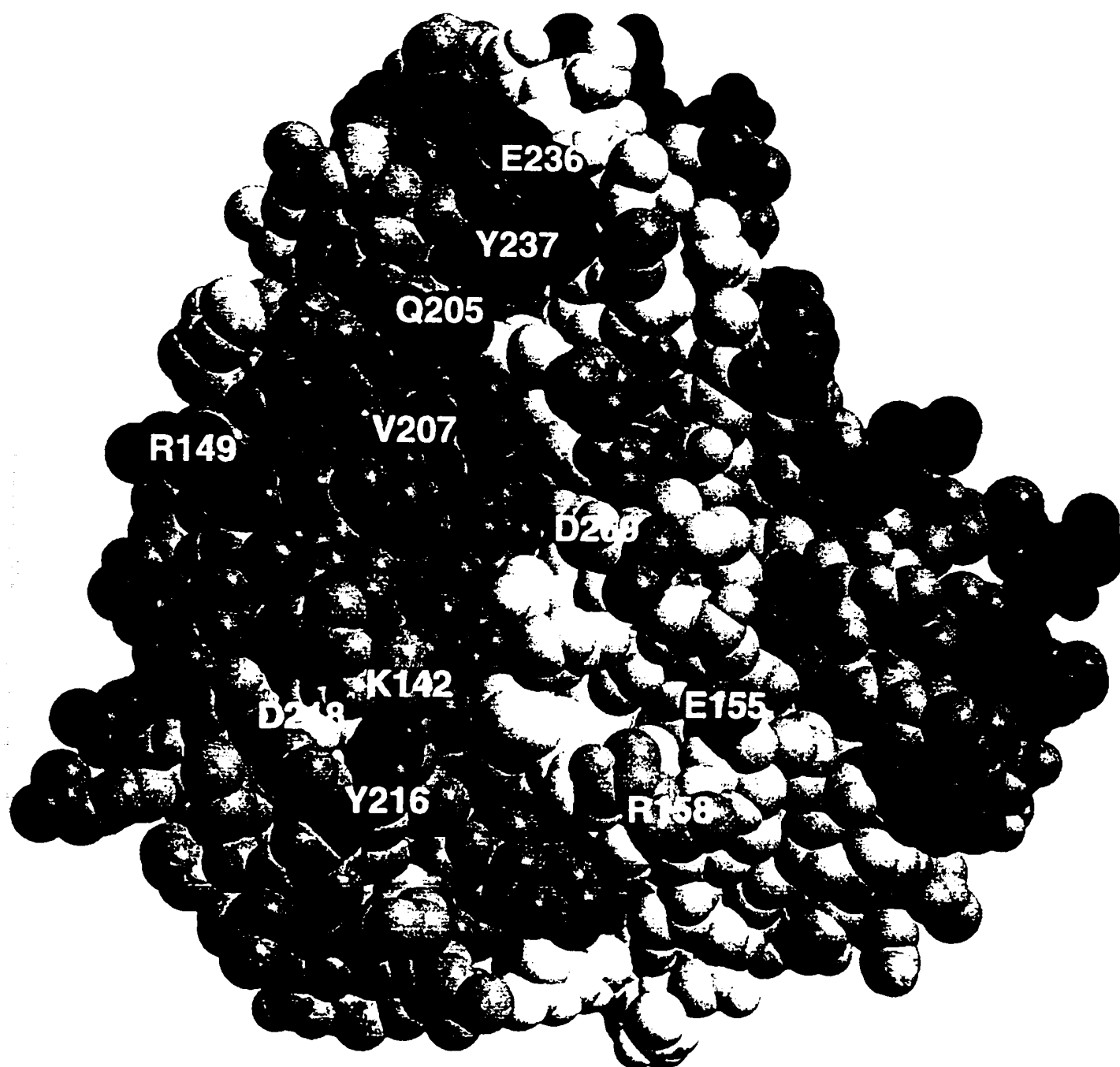


Figure 5

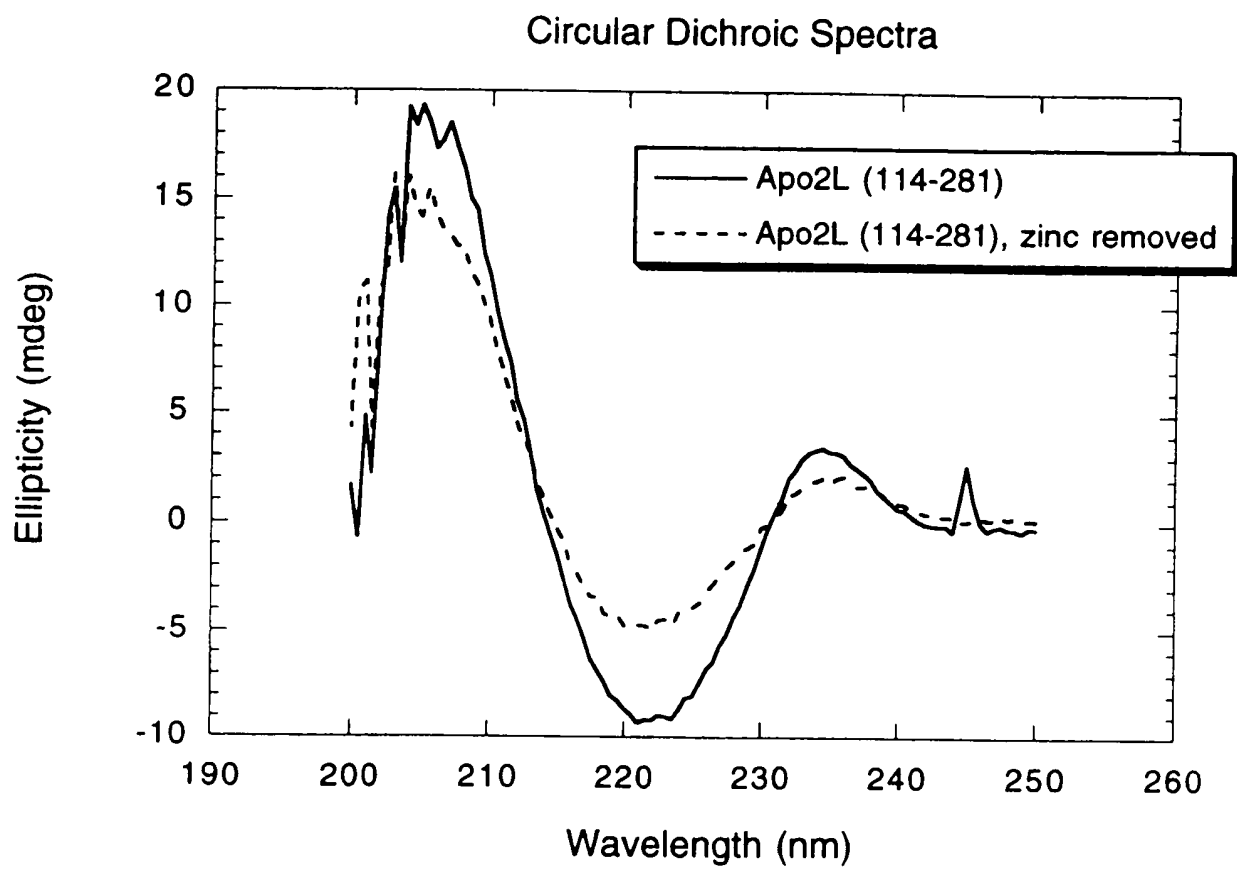


Fig. 6

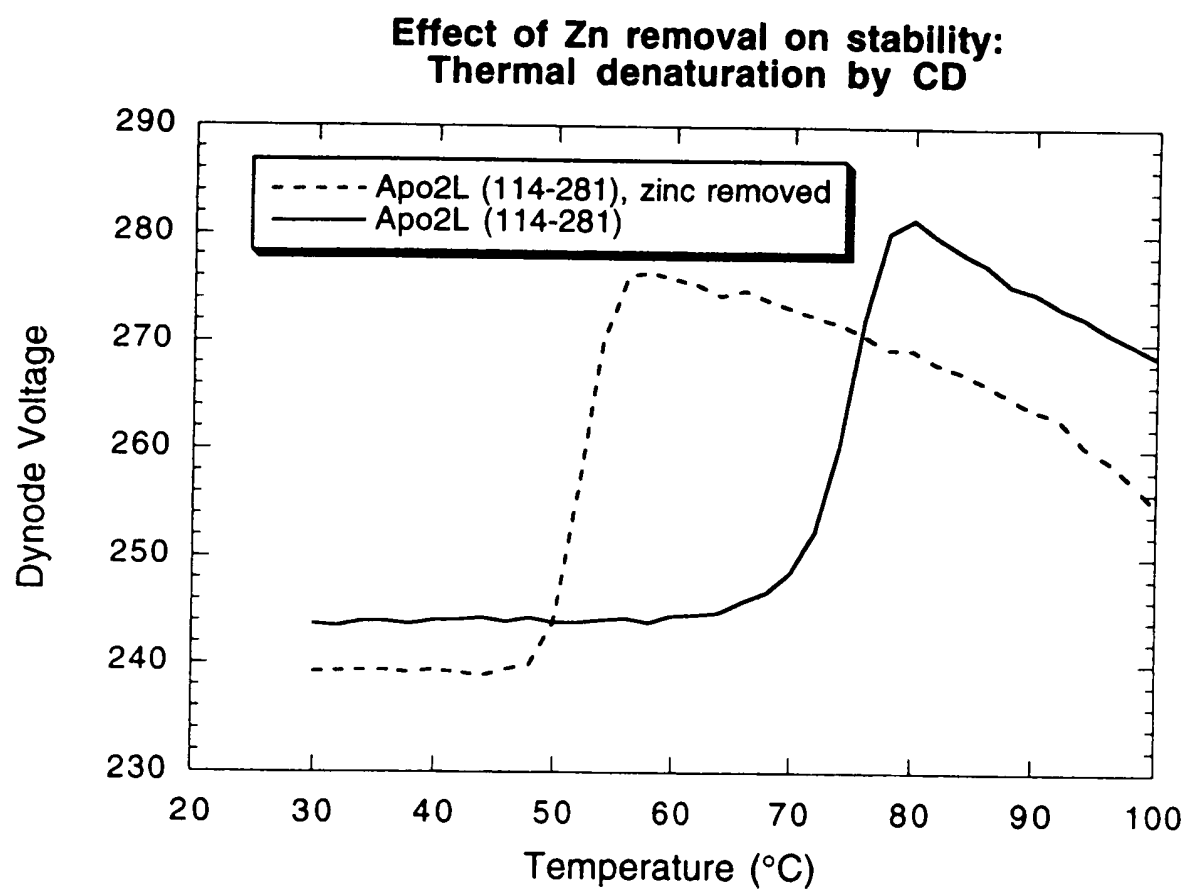


Fig. 7

Effect of ZnSO₄ Additions on Apo2L Product Accumulation

(E. coli W3110 fhuA (tonA) phoA Δ(argF-lac) degP⁻ kds⁻ ompT livG⁺)
 Production Host: 43E7

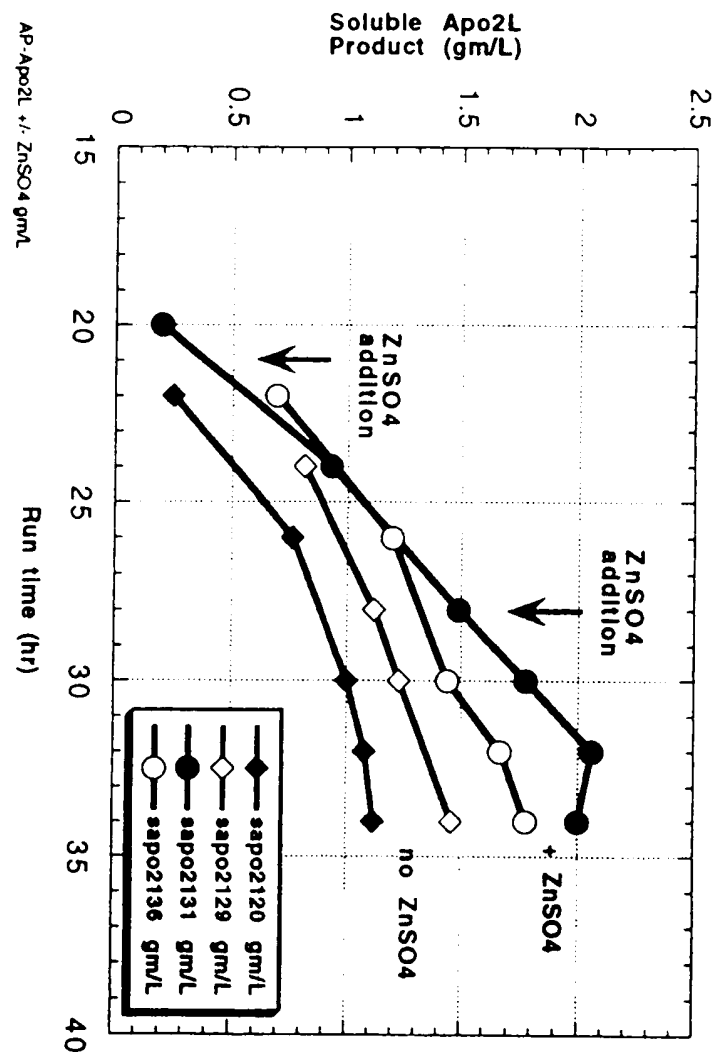
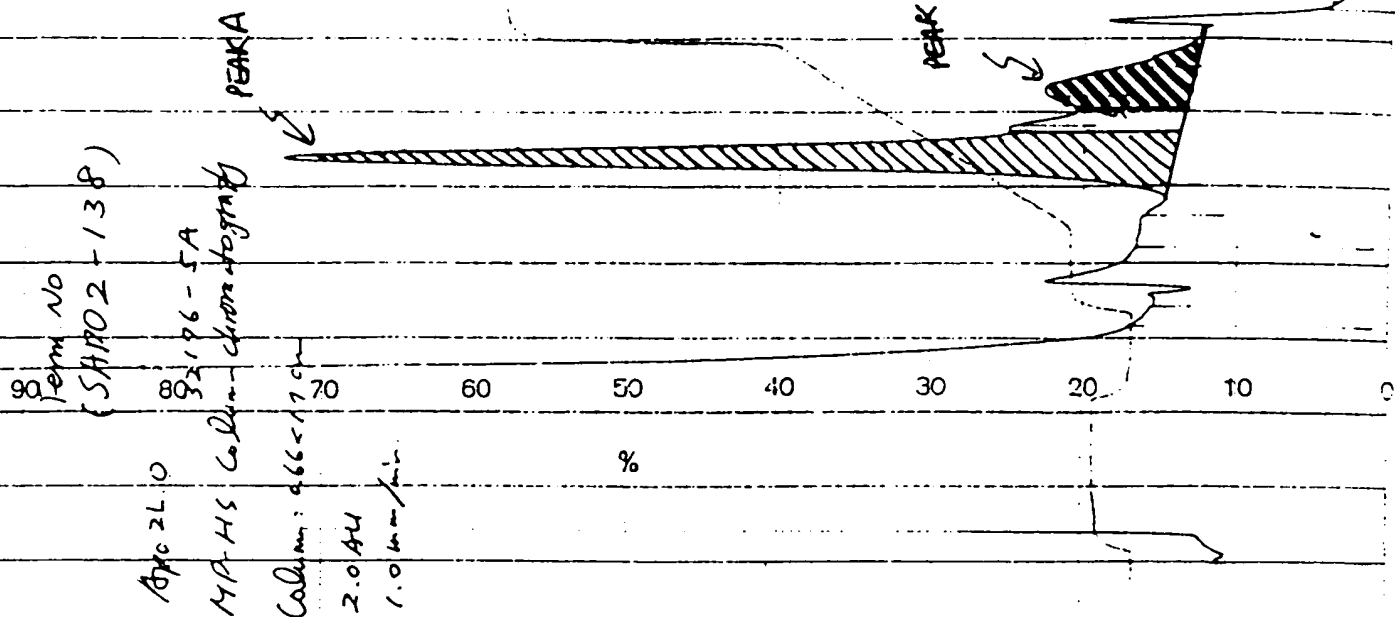
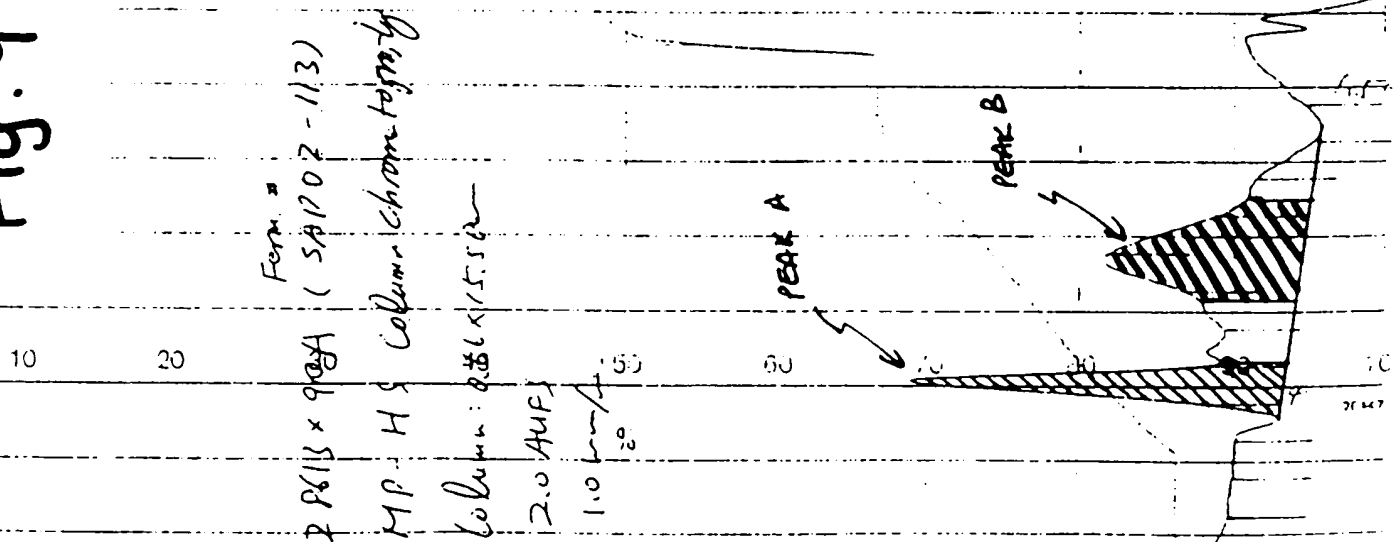
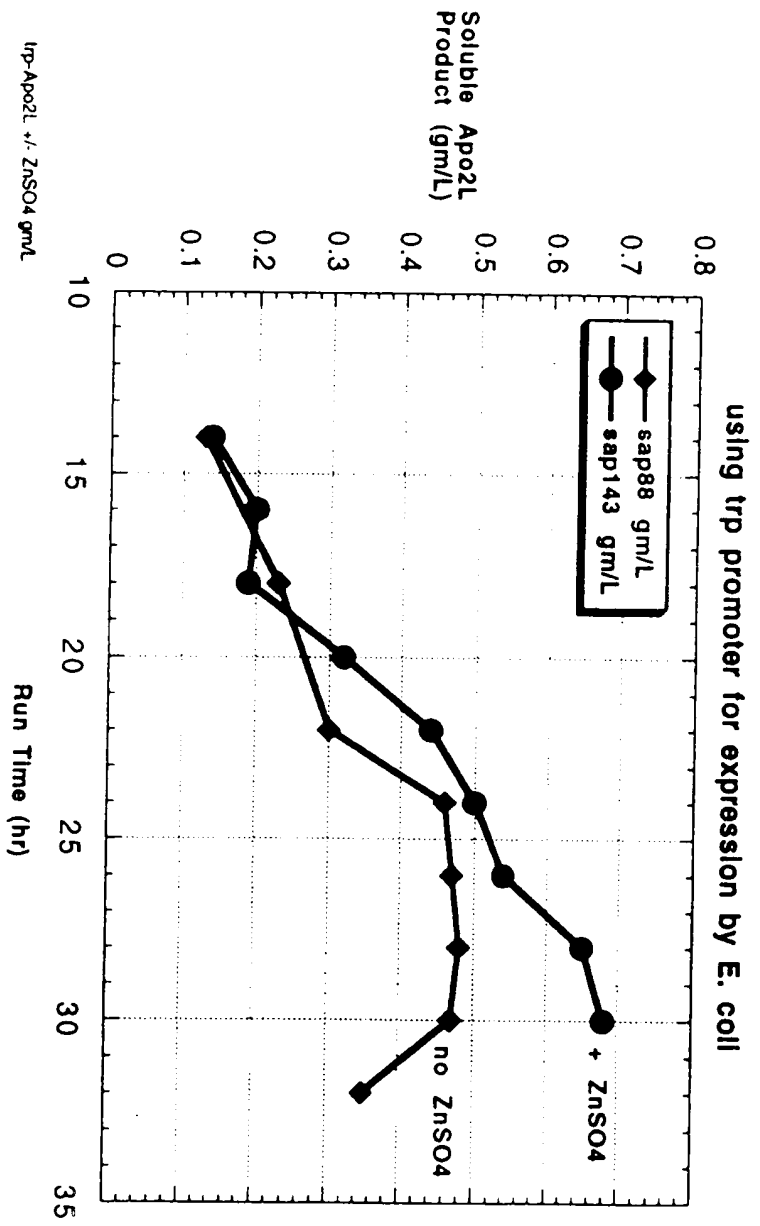


Fig. 8

Fig. 9



Effect of ZnSO4 Additions on Apo2L Product Accumulation



Effect of Coc12 additions on Apo2L Product Accumulation

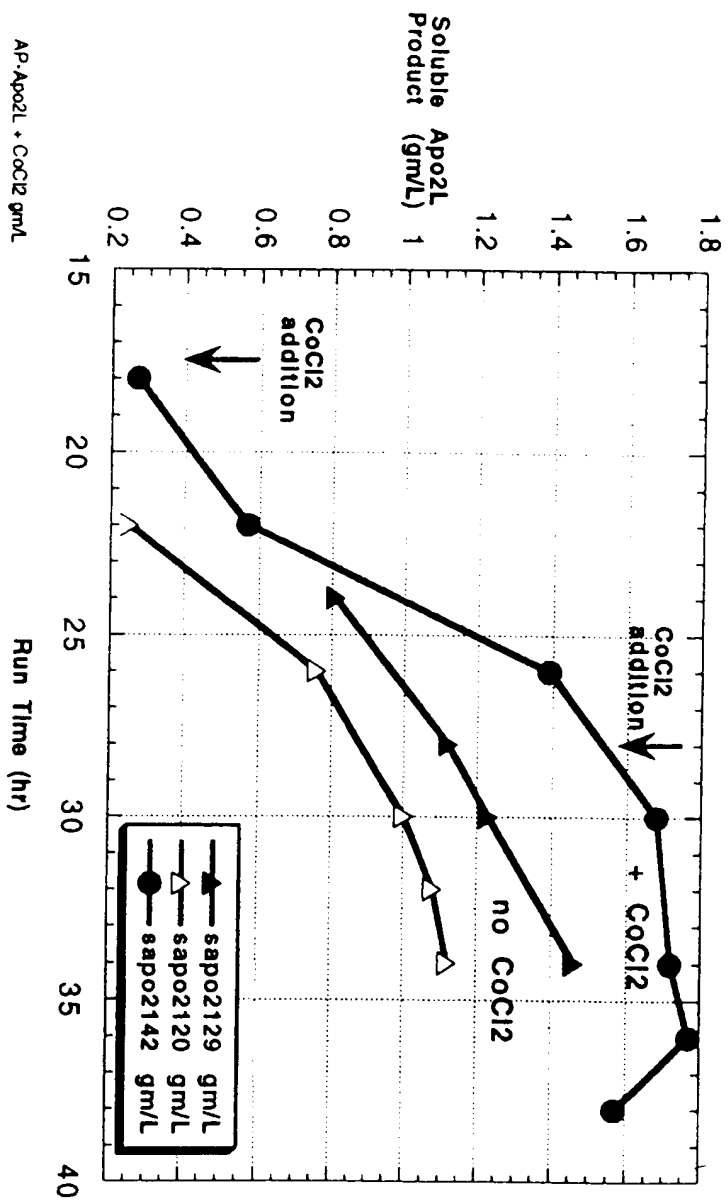


Fig. 11

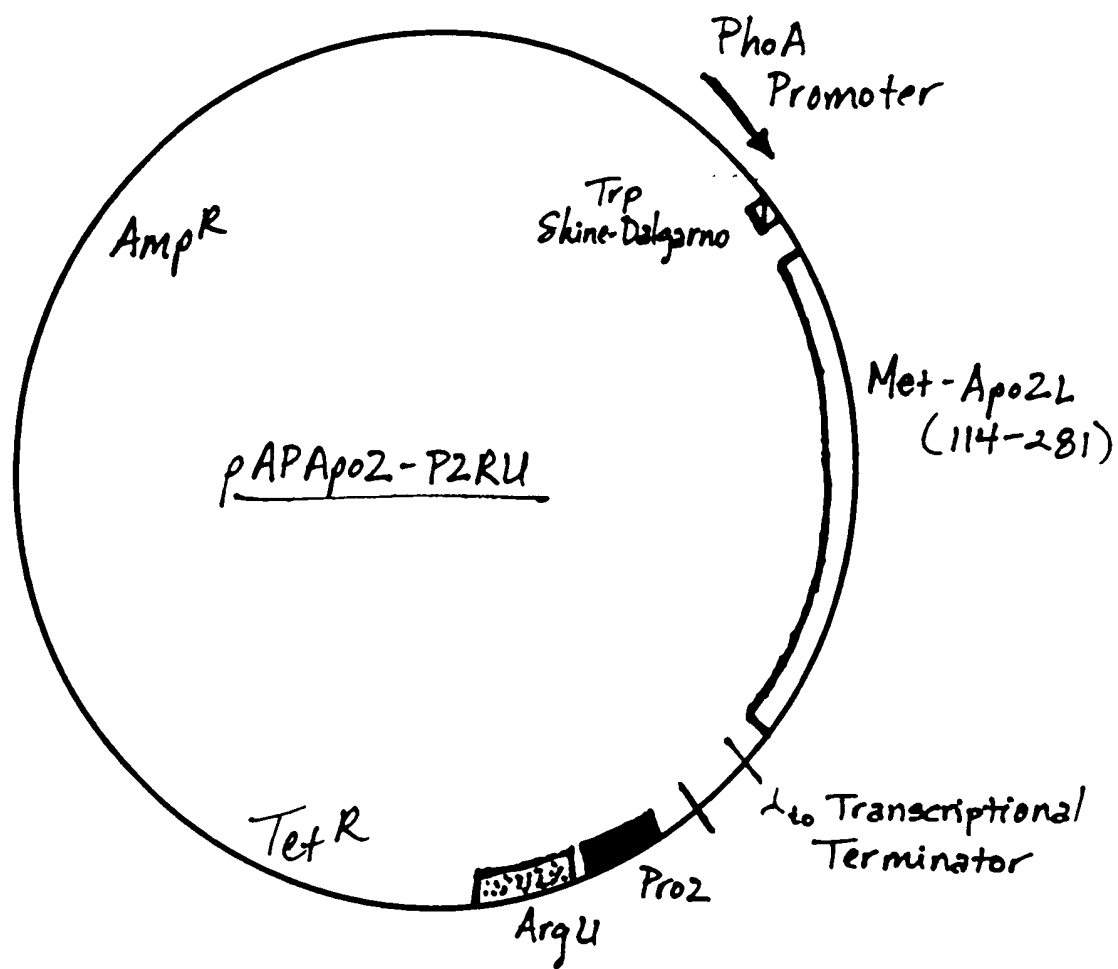


Fig. 12

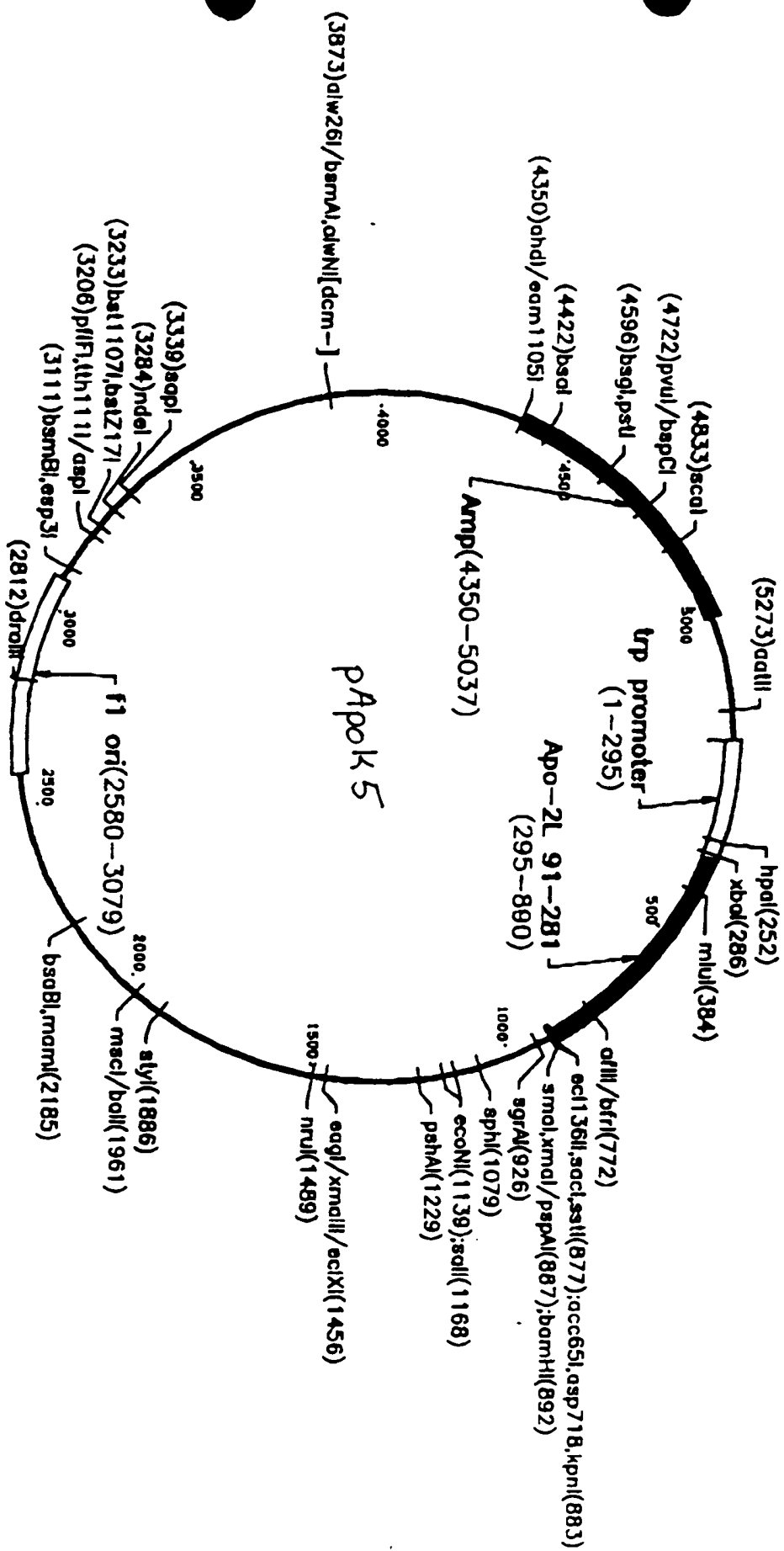


Fig. 13